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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=11; day=24; hr=14; min=36; sec=6; ms=951; ]

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Application No: 10551667

Version No: 1.0

Input Set:

Output Set:

Started: 2008-11-03 14:18:58.775

Finished: 2008-11-03 14:19:01.599

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 824 ms

Total Warnings: 79

Total Errors: 0

No. of SeqIDs Defined: 111

Actual SeqID Count: 111

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
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W 213	Artificial or Unknown found in <213> in SEQ ID (15)
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W 213	Artificial or Unknown found in <213> in SEQ ID (43)
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**Input Set:**

**Output Set:**

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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 251	Found intentionally skipped sequence in SEQID (70 )
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W 251	Found intentionally skipped sequence in SEQID (75 )

# SEQUENCE LISTING

<110> LU, PATRICK Y.  
XIE, FRANK Y.  
WOODLE, MARTIN C.  
LIU, YIJIN  
TANG, QUINN Q.  
XU, JUN

<120> TARGETS FOR TUMOR GROWTH INHIBITION

<130> INTM/017

<140> 10551667

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<150> PCT/US04/010059

<151> 2004-04-01

<150> 60/458,948

<151> 2003-08-01

<150> 60/489,504

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<160> 111

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<210> 2

<211> 387

<212> PRT

<213> Homo sapiens

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```

```

His Asn Gly Gly Leu Cys Glu Glu Ile Ser Gln Glu Val Arg Gly Asp
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```

```

Val Phe Pro Ser Tyr Thr Cys Thr Cys Leu Lys Gly Tyr Ala Gly Asn
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```

```

His Cys Glu Thr Lys Cys Val Glu Pro Leu Gly Met Glu Asn Gly Asn
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```

```

Ile Ala Asn Ser Gln Ile Ala Ala Ser Ser Val Arg Val Thr Phe Leu
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Gly Leu Gln His Trp Val Pro Glu Leu Ala Arg Leu Asn Arg Ala Gly
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```

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```

Gln Val Asn Leu Leu Arg Arg Met Trp Val Thr Gly Val Val Thr Gln
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Gly Ala Ser Arg Leu Ala Ser His Glu Tyr Leu Lys Ala Phe Lys Val
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Ala Tyr Ser Leu Asn Gly His Glu Phe Asp Phe Ile His Asp Val Asn
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Lys Lys His Lys Glu Phe Val Gly Asn Trp Asn Lys Asn Ala Val His
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195

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205

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Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr Trp Gly  
 245 250 255

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 260 265 270

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Leu Gln Val Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr  
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Gln Gly Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys  
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Val Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro  
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His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg Tyr Val Arg  
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Leu Gly Cys  
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<211> 1164

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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35 40 45

Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg  
50 55 60

Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp  
65 70 75 80

Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn  
85 90 95

Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys  
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Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys  
115 120 125

Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg  
130 135 140

Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala  
145 150 155 160

Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe  
165 170 175

Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr  
180 185 190

Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr  
195 200 205

Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile  
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<212> DNA

<213> Homo sapiens

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<210> 7

<211> 472

<212> PRT

<213> Homo sapiens

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```

```

Val Pro Asn Phe His Lys Cys Glu Ile Cys Leu Leu Ser Phe Pro Lys
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```

```

Glu Ser Gln Phe Gln Arg His Met Arg Asp His Glu Arg Asn Asp Lys
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```

Pro His Arg Cys Asp Gln Cys Pro Gln Thr Phe Asn Val Glu Phe Asn  
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Leu Thr Leu His Lys Cys Thr His Ser Gly Glu Asp Pro Thr Cys Pro  
85 90 95

Val Cys Asn Lys Lys Phe Ser Arg Val Ala Ser Leu Lys Ala His Ile  
100 105 110

Met Leu His Glu Lys Glu Glu Asn Leu Ile Cys Ser Glu Cys Gly Gly  
115 120 125

Glu Phe Thr Leu Gln Ser Gln Leu Ala Val His Met Glu Glu His Arg  
130 135 140

Gln Glu Leu Ala Gly Thr Arg Gln His Ala Cys Lys Ala Cys Lys Lys  
145 150 155 160

Glu Phe Glu Thr Ser Ser Glu Leu Lys Glu His Met Lys Thr His Tyr  
165 170 175

Lys Ile Arg Val Ser Ser Thr Arg Ser Tyr Asn Arg Asn Ile Asp Arg  
180 185 190

Ser Gly Phe Thr Tyr Ser Cys Pro His Cys Gly Lys Thr Phe Gln Lys  
195 200 205

Pro Ser Gln Leu Thr Arg His Ile Arg Ile His Thr Gly Glu Arg Pro  
210 215 220

Phe Lys Cys Ser Glu Cys Gly Lys Ala Phe Asn Gln Lys Gly Ala Leu  
225 230 235 240

Gln Thr His Met Ile Lys His Thr Gly Glu Lys Pro His Ala Cys Ala  
245 250 255

Phe Cys Pro Ala Ala Phe Ser Gln Lys Gly Asn Leu Gln Ser His Val  
260 265 270

Gln